

SEQUENCE LISTING

<110> BIOGEN, INC.

<120> THERAPIES FOR RENAL FAILURE USING INTERFERON-BETA

<130> BII-001.25

<140> PCT/US03/22440

<141> 2003-07-17

<150> US 60/396,393

<151> 2002-07-17

<160> 21

<170> PatentIn Ver. 2.1

<210> 1

<211> 840

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (76)..(636)

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gttcgtgttg tcaac atg acc aac aag tgt ctc ctc caa att gct ctc ctg 111
Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu
1 5 10

ttg tgc ttc tcc act aca gct ctt tcc atg agc tac aac ttg ctt gga 159
Leu Cys Phe Ser Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly
15 20 25

ttc cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa 207
Phe Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln
30 35 40

ttg aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac 255
Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp
45 50 55 60

atc cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc 303
Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala
65 70 75

gca ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga 351
Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg
80 85 90

caa gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc 399
Gln Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu
95 100 105

ctg gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa 447
 Leu Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu
 110 115 120

 gaa aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt 495
 Glu Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser
 125 130 135 140

 ctg cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc 543
 Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala
 145 150 155

 aag gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta 591
 Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu
 160 165 170

 agg aac ttt tac ttc att aac aga ctt aca ggt tac ctc cga aac 636
 Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 175 180 185

 tgaagatctc ctagcctgtg cctctgggac tggacaattg cttcaagcat tcttcaacca 696
 gcagatgctg ttttaagtgc tgatggctaa tgtactgcat atgaaaggac actagaagat 756
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 aaattatttt tgggtgcaaaa gtca 840

<210> 2
 <211> 187
 <212> PRT
 <213> Homo sapiens

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 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
 20 25 30

 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125
 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140
 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
 145 150 155 160
 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
 165 170 175
 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
 180 185

<210> 3
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(498)

<400> 3
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 Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
 1 5 10 15
 tgt cag aag ctc ctg tgg caa ttg aat ggg agg ctt gaa tac tgc ctc 96
 Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu
 20 25 30
 aag gac agg atg aac ttt gac atc cct gag gag att aag cag ctg cag 144
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 cag ttc cag aag gag gac gcc gca ttg acc atc tat gag atg ctc cag 192
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 aac atc ttt gct att ttc aga caa gat tca tct agc act ggc tgg aat 240
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 gag act att gtt gag aac ctc ctg gct aat gtc tat cat cag ata aac 288
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 cat ctg aag aca gtc ctg gaa gaa aaa ctg gag aaa gaa gat ttc acc 336
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110
 agg gga aaa ctc atg agc agt ctg cac ctg aaa aga tat tat ggg agg 384

Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 att ctg cat tac ctg aag gcc aag gag tac agt cac tgt gcc tgg acc 432
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 ata gtc aga gtg gaa atc cta agg aac ttt tac ttc att aac aga ctt 480
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 aca ggt tac ctc cga aac tga 501
 Thr Gly Tyr Leu Arg Asn
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 <210> 4
 <211> 166
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln
 35 40 45
 Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln
 50 55 60
 Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser Ser Thr Gly Trp Asn
 65 70 75 80
 Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val Tyr His Gln Ile Asn
 85 90 95
 His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp Phe Thr
 100 105 110
 Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg
 115 120 125
 Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr
 130 135 140
 Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu
 145 150 155 160
 Thr Gly Tyr Leu Arg Asn
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<210> 5
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker
oligonucleotide

<400> 5
ggcggtggtg gcagc

15

<210> 6
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Linker peptide

<400> 6
Gly Gly Gly Gly Ser
1 5

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Enterokinase
recognition site oligonucleotide

<400> 7
gacgatgatg acaag

15

<210> 8
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Enterokinase
recognition site

<400> 8
Asp Asp Asp Asp Lys
1 5

<210> 9
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Modified enterokinase
        recognition site oligonucleotide

<400> 9
agctccggag acgatgatga caag                                24

<210> 10
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Modified
        enterokinase recognition site

<400> 10
Ser Ser Gly Asp Asp Asp Asp Lys
 1                      5

<210> 11
<211> 1257
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1254)

<220>
<223> Description of Artificial Sequence: Synthetic
        IFN-beta G162C-Ig direct fusion construct nucleotide
        sequence

<400> 11
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Met Pro Gly Lys Met Val Val Ile Leu Gly Ala Ser Asn Ile Leu Trp
 1                      5                      10                      15

ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc      96
Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe
                20                      25                      30

cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg      144
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
                35                      40                      45

aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc      192
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
                50                      55                      60

cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca      240
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala
 65                      70                      75                      80

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ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa	288
Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln	
85 90 95	
gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg	336
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu	
100 105 110	
gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa	384
Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu	
115 120 125	
aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg	432
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu	
130 135 140	
cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag	480
His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys	
145 150 155 160	
gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg	528
Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg	
165 170 175	
aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac gtc gac	576
Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp	
180 185 190	
aaa act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga	624
Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly	
195 200 205	
ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc	672
Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile	
210 215 220	
tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa	720
Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu	
225 230 235 240	
gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat	768
Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His	
245 250 255	
aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac cgt	816
Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg	
260 265 270	
gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag	864
Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys	
275 280 285	
gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag	912
Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu	
290 295 300	

aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac	960
Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr	
305 310 315 320	
acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc ctg	1008
Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu	
325 330 335	
acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg	1056
Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp	
340 345 350	
gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg	1104
Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val	
355 360 365	
ttg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac	1152
Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp	
370 375 380	
aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat	1200
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His	
385 390 395 400	
gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct ccc	1248
Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro	
405 410 415	
ggg aaa tga	1257
Gly Lys	

<210> 12
 <211> 418
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 IFN-beta G162C-Ig direct fusion construct protein

<400> 12	
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Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe	
20 25 30	
Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu	
35 40 45	
Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile	
50 55 60	
Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala	
65 70 75 80	

Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 85 90 95
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu
 100 105 110
 Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu
 115 120 125
 Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu
 130 135 140
 His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys
 145 150 155 160
 Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg
 165 170 175
 Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Val Asp
 180 185 190
 Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly
 195 200 205
 Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile
 210 215 220
 Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu
 225 230 235 240
 Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His
 245 250 255
 Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg
 260 265 270
 Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys
 275 280 285
 Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu
 290 295 300
 Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr
 305 310 315 320
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 325 330 335
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 340 345 350
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 355 360 365
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 370 375 380

Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 385 390 395 400

Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 405 410 415

Gly Lys

<210> 13
 <211> 1272
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1269)

<220>
 <223> Description of Artificial Sequence: Synthetic
 IFN-beta G162C-Ig fusion construct nucleotide sequence

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 ata atg ttt gca gct tct caa gcc atg agc tac aac ttg ctt gga ttc 96
 Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe
 20 25 30
 cta caa aga agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg 144
 Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
 35 40 45
 aat ggg agg ctt gaa tac tgc ctc aag gac agg atg aac ttt gac atc 192
 Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
 50 55 60
 cct gag gag att aag cag ctg cag cag ttc cag aag gag gac gcc gca 240
 Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala
 65 70 75 80
 ttg acc atc tat gag atg ctc cag aac atc ttt gct att ttc aga caa 288
 Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 85 90 95
 gat tca tct agc act ggc tgg aat gag act att gtt gag aac ctc ctg 336
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu
 100 105 110
 gct aat gtc tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa 384
 Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu
 115 120 125

aaa ctg gag aaa gaa gat ttc acc agg gga aaa ctc atg agc agt ctg	432
Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu	
130 135 140	
cac ctg aaa aga tat tat ggg agg att ctg cat tac ctg aag gcc aag	480
His Leu Lys Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys	
145 150 155 160	
gag tac agt cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg	528
Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg	
165 170 175	
aac ttt tac ttc att aac aga ctt aca tgt tac ctc cga aac ggc ggt	576
Asn Phe Tyr Phe Ile Asn Arg Leu Thr Cys Tyr Leu Arg Asn Gly Gly	
180 185 190	
ggt ggc agc gtc gac aaa act cac aca tgc cca ccg tgc cca gca cct	624
Gly Gly Ser Val Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro	
195 200 205	
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag	672
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys	
210 215 220	
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg	720
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val	
225 230 235 240	
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac	768
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp	
245 250 255	
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac	816
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr	
260 265 270	
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac	864
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp	
275 280 285	
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc	912
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu	
290 295 300	
cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga	960
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg	
305 310 315 320	
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag	1008
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys	
325 330 335	
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac	1056
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp	
340 345 350	

atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag 1104
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
 355 360 365
 acc acg cct ccc gtg ttg gac tcc gac ggc tcc ttc ttc ctc tac agc 1152
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
 370 375 380
 aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca 1200
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
 385 390 395 400
 tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc 1248
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
 405 410 415
 ctc tcc ctg tct ccc ggg aaa tga 1272
 Leu Ser Leu Ser Pro Gly Lys
 420

<210> 14
 <211> 423
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 IFN-beta G162C-Ig fusion construct protein

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 Ile Met Phe Ala Ala Ser Gln Ala Met Ser Tyr Asn Leu Leu Gly Phe
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 Leu Gln Arg Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu
 35 40 45
 Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile
 50 55 60
 Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala
 65 70 75 80
 Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
 85 90 95
 Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu
 100 105 110
 Ala Asn Val Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu
 115 120 125
 Lys Leu Glu Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu
 130 135 140

His	Leu	Lys	Arg	Tyr	Tyr	Gly	Arg	Ile	Leu	His	Tyr	Leu	Lys	Ala	Lys	145	150	155	160
Glu	Tyr	Ser	His	Cys	Ala	Trp	Thr	Ile	Val	Arg	Val	Glu	Ile	Leu	Arg	165	170	175	
Asn	Phe	Tyr	Phe	Ile	Asn	Arg	Leu	Thr	Cys	Tyr	Leu	Arg	Asn	Gly	Gly	180	185	190	
Gly	Gly	Ser	Val	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	195	200	205	
Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	210	215	220	
Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	225	230	235	240
Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	245	250	255	
Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	260	265	270	
Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	275	280	285	
Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	290	295	300	
Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	305	310	315	320
Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	325	330	335	
Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	340	345	350	
Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	355	360	365	
Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	370	375	380	
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	385	390	395	400
Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	405	410	415	
Leu	Ser	Leu	Ser	Pro	Gly	Lys										420			

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18

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